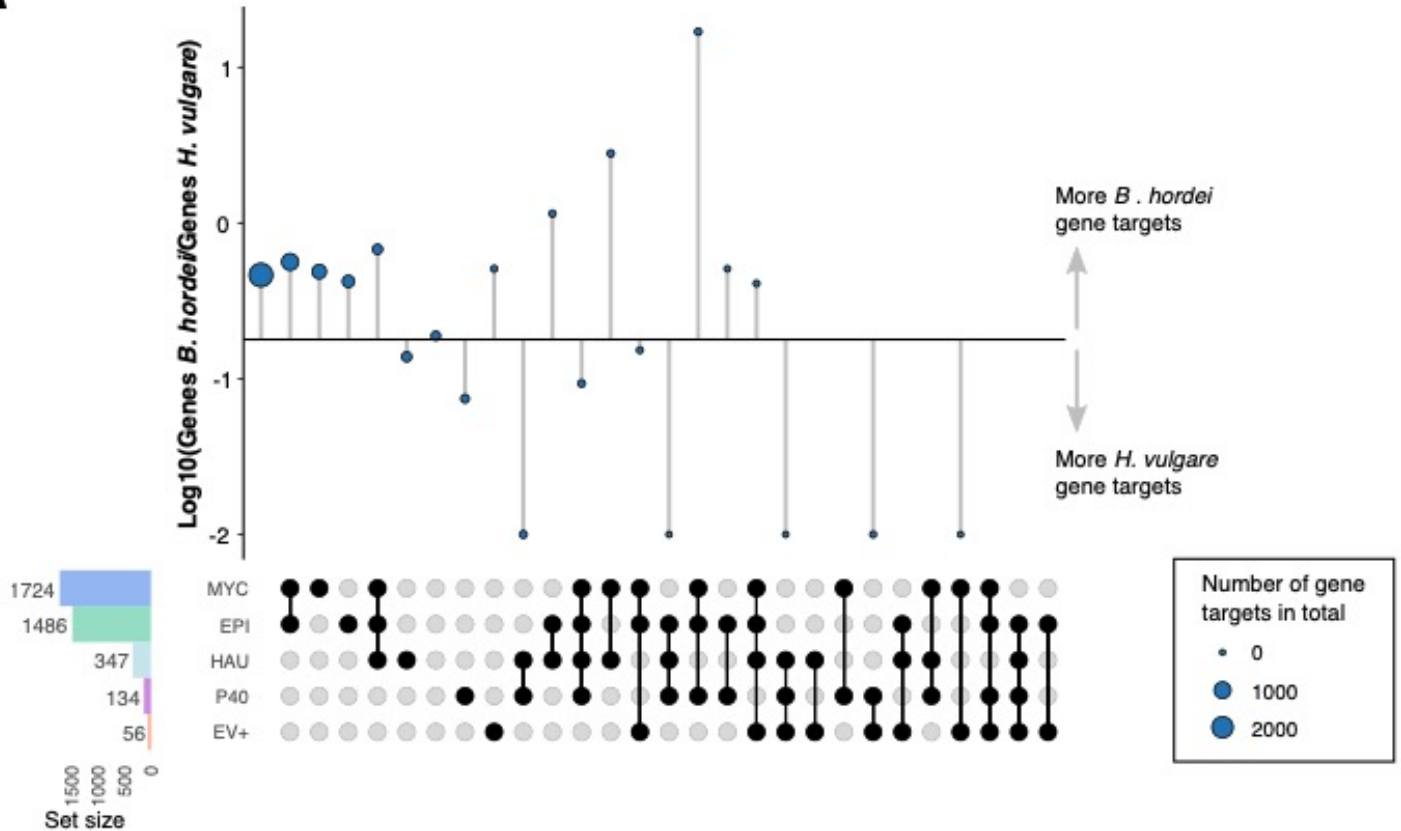
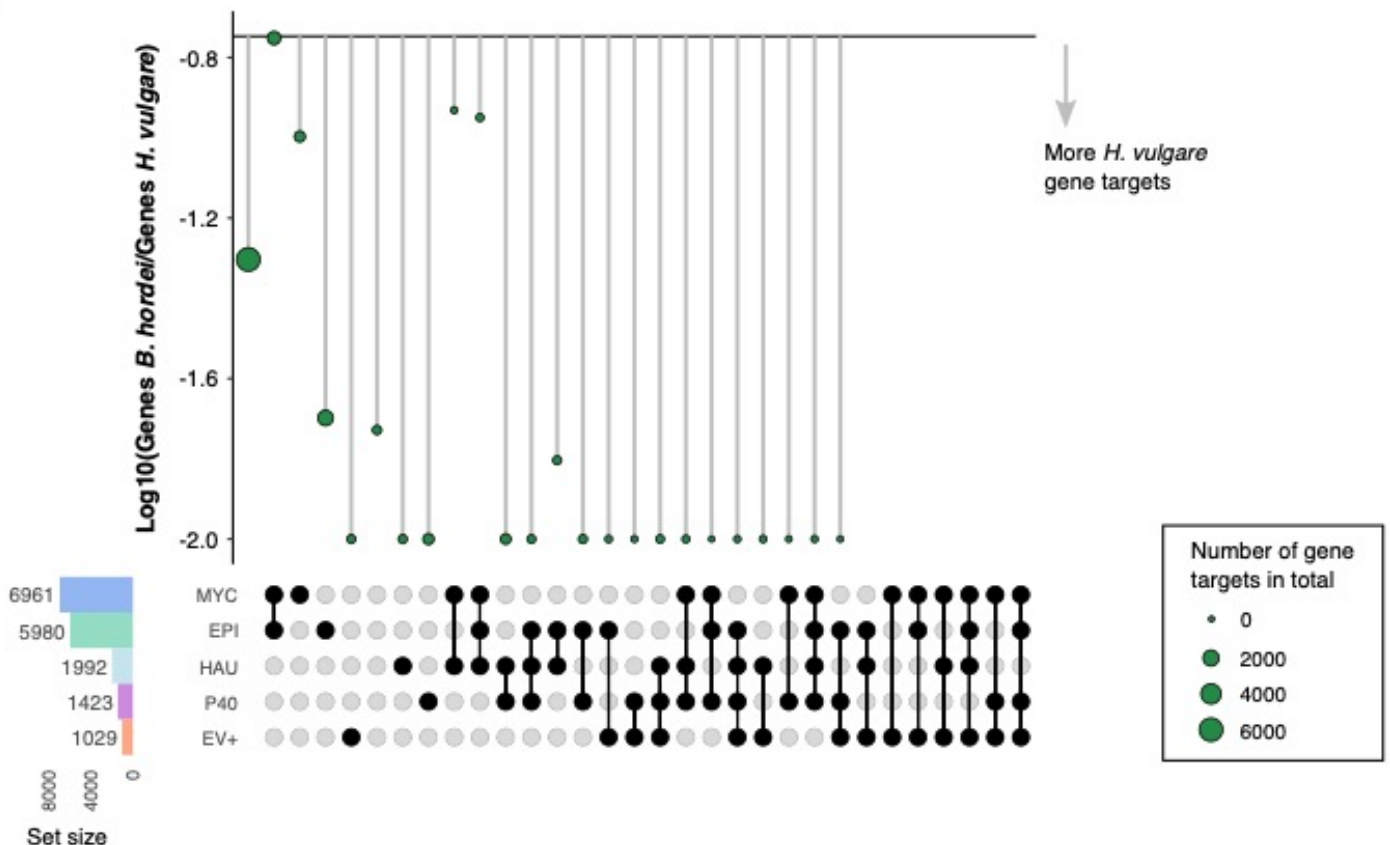


A**B**

Supplementary Figure 11. Subsets of miRNAs preferentially target *B. hordei* or *H. vulgare* genes. We calculated the ratio of *B. hordei* target genes divided by *H. vulgare* target genes of the entire transcriptomes (7,137 in case of *B. hordei* and 39,734 for *H. vulgare*) and the respective subsets of *B. hordei* (A) and *H. vulgare* (B) miRNAs (Figure 5). The plots show the Log10+0.01 values of these ratios (y-axis) for each subset (x-axis). The left-most data point indicates the ratio of the entire set of miRNA targets. Missing data points are due to lacking predicted target genes of the respective miRNA sets.